



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/509,249
Source: PCT
Date Processed by STIC: 10-04-2004

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/509,249

DATE: 10/04/2004

TIME: 12:16:23

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509249.raw

3 <110> APPLICANT: Japan Science and Technology Corporation
 5 <120> TITLE OF INVENTION: Antibodies presented protein hollow nano-particles for therapeutic drug
 6 and protein hollow nano-particles.
 8 <130> FILE REFERENCE: P023P03
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,249
 C--> 10 <141> CURRENT FILING DATE: 2004-09-28
 10 <150> PRIOR APPLICATION NUMBER: JP 2002-97424
 W--> 11 <151> PRIOR FILING DATE: 2002-3-29
 13 <150> PRIOR APPLICATION NUMBER: JP 2003-045088
 W--> 14 <151> PRIOR FILING DATE: 2003-2-21
 16 <160> NUMBER OF SEQ ID NOS: 29
 18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 39
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 W--> 24 <220> FEATURE: Synthesized Oligonucleotide
 W--> 25 <223> OTHER INFORMATION:
 W--> 25 <400> SEQUENCE: 1
 E--> 26 cgacaaggca tgggaggcgg cgcgagcct caggctcag????????39
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 39
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Artificial Sequence
 W--> 32 <220> FEATURE: Synthesized Oligonucleotide
 W--> 33 <223> OTHER INFORMATION:
 W--> 33 <400> SEQUENCE: 2
 E--> 34 ctgagcctga gggctgccc cgcctcccat gccttgctg????????39
 68 <210> SEQ ID NO: 7
 69 <211> LENGTH: 29
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Artificial Sequence
 W--> 72 <220> FEATURE: Synthesized Oligonucleotide
 W--> 73 <223> OTHER INFORMATION:
 W--> 73 <400> SEQUENCE: 7
 E--> 74 ggggtaccat gagatctttg ttgatcttg????????????29
 76 <210> SEQ ID NO: 8
 77 <211> LENGTH: 28
 78 <212> TYPE: DNA

MANDATORY, section
 (220) is to be
 kept blank at all
 times.

Does Not Comply
 Corrected Diskette Needed
 (pg. 1-2)

pls insert

Insert into section
 (223).

delete

Insert into section (223)

delete

same errors

↑ pls see error explanation
 on page 3.

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79 <213> ORGANISM: Artificial Sequence
W--> 80 <220> FEATURE: Synthesized Oligonucleotide
W--> 81 <223> OTHER INFORMATION:
W--> 81 <400> SEQUENCE: 8
E--> 82 ggccgcggtt aaatgtatac ccaaagac???????????? 28

same errors

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
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Use of <220> Feature (NEW RULES):

Error Explanation:

~~Sequence is missing the <220> Feature and associated headings~~
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26

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Input Set : A:\PTO.FG.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:24 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:25 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:25 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:39 Counted:47 SEQ:1
L:26 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:26 M:252 E: No. of Seq. differs, <211> LENGTH:Input:39 Found:47 SEQ:1
L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:33 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:33
L:34 M:254 E: No. of Bases conflict, LENGTH:Input:39 Counted:47 SEQ:2
L:34 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:34 M:252 E: No. of Seq. differs, <211> LENGTH:Input:39 Found:47 SEQ:2
L:40 M:283 W: Missing Blank Line separator, <220> field identifier
L:40 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:41 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:41 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:41
L:48 M:283 W: Missing Blank Line separator, <220> field identifier
L:48 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:49 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:49
L:56 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:57 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:57 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:57
L:64 M:283 W: Missing Blank Line separator, <220> field identifier
L:64 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:65 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:65 M:283 W: Missing Blank Line separator, <400> field identifier
L:65 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:65
L:72 M:283 W: Missing Blank Line separator, <220> field identifier
L:72 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:73 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:73 M:283 W: Missing Blank Line separator, <400> field identifier
L:73 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:73
L:74 M:254 E: No. of Bases conflict, LENGTH:Input:29 Counted:43 SEQ:7

L:74 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14

L:74 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:43 SEQ:7 ✓

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L:80 M:283 W: Missing Blank Line separator, <220> field identifier
L:80 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:81 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:81 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:81
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:28 Counted:42 SEQ:8
L:82 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:82 M:252 E: No. of Seq. differs, <211> LENGTH:Input:28 Found:42 SEQ:8
L:88 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:89 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:89
L:96 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:97 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:97 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:97
L:104 M:283 W: Missing Blank Line separator, <220> field identifier
L:104 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:105 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:105
L:112 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:113 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:113 M:283 W: Missing Blank Line separator, <400> field identifier
L:113 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:113
L:120 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:121 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:121 M:283 W: Missing Blank Line separator, <400> field identifier
L:121 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:121
L:128 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:129 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:129 M:283 W: Missing Blank Line separator, <400> field identifier
L:129 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:129
L:136 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:137 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:137
L:144 M:283 W: Missing Blank Line separator, <220> field identifier
L:144 M:256 W: Invalid Numeric Header Field, <220> has non-blank data

L:145 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:145 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:145
L:152 M:283 W: Missing Blank Line separator, <220> field identifier

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L:152 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:153 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:153 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:153
L:160 M:283 W: Missing Blank Line separator, <220> field identifier
L:160 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:161 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
ORGANISM:Artificial Sequence
L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:161 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:161
L:168 M:283 W: Missing Blank Line separator, <220> field identifier
L:168 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:169 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:169 M:283 W: Missing Blank Line separator, <400> field identifier
L:169 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:169
L:176 M:283 W: Missing Blank Line separator, <220> field identifier
L:176 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:177 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:177
L:184 M:283 W: Missing Blank Line separator, <220> field identifier
L:184 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:185 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:185 M:283 W: Missing Blank Line separator, <400> field identifier
L:185 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:185
L:192 M:283 W: Missing Blank Line separator, <220> field identifier
L:192 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:193 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:193 M:283 W: Missing Blank Line separator, <400> field identifier
L:193 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:193
L:200 M:283 W: Missing Blank Line separator, <220> field identifier
L:200 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:201 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:201 M:283 W: Missing Blank Line separator, <400> field identifier
L:201 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:201
L:208 M:283 W: Missing Blank Line separator, <220> field identifier
L:208 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:209 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:209 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:209
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:216 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:217 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:217 M:283 W: Missing Blank Line separator, <400> field identifier
L:217 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:217

L:224 M:256 W: Invalid Numeric Header Field, <220> has non-blank data